Figure 1.

A.

R1

| 1 | 212 | 959 | 1362 | 1726 | 2122 nt |

N-glyco   N-glyco   N-glyco   N-glyco

ORF coding capacity = 504 aa

PEDF binding region = clone 12

TM domain

B.

hydrophobicity value

upper cutoff
lower cutoff

aa start position of window in sequence

C.

Extracellular

Intracellular

1D — 178 Patatin-like Domain

Figure 1.

D.

```
R1          MFPREKTWNISFAGCGFLGVYYVGVASCLREHAPFLVANATHIYGASAGALTATALVTGVCLGEAGAKFIEVSKEARKRFLG
adiponutrin YDA RG SL  F H ATR      H LRD RMLF  HCVGVLS I P EQTLQVLISDLVRK  S NI

            PLHPSFNLVKIIRSFLLKVLPADSHEHASGRLGISLTRVSDGENVIISHFNSKDELIQANVCSGFIPVYCGLIPPSLQGVRYV
            IF   S FL QG C C  NV QLI KI          LV DFR         VVD  L C F S   FR

            DGGISDNLPLYELKNTITVSPFSGESDICPQDSSTNIHELRVTNTSIQFNLRNLYRLSKA LFPPEPLVLREMCKQGYRDGLR
            V V FIDA T    P Y Y  KVK    FLHVDI KL LRLCTG   L R  FV DLK  G I LR  L AF

            FLQRNGLLNRPNP-LLALPP----------------ARPHGPEDKDQAVESAQAE--DYSQLP--GEDH-ILEHLPARLNEALLE
            EEK IC    Q G KSSSEGMDPEVAMPSWANMSLDSS SAAL  RLEGD LL HLR SILPW ES  DT SP AT S

            ACVEPTDLITTLSNMLPVRLATAMMVPYTLPLESALSFTIRLLEWLPDVPEDIRWMKEQT GSICQ YLVMRAKRKLGRHLPS
            EMKDKGGYMSKIC L I IMSYV L C  V IAIVQ    VT    M D VL LQWV  SQVFTRVL CLLPASRSQM V

            RLPEQVELRRVQSLIPS-VPLSCAAYREALPGWMRNNLSLGDALAKWEECQRQLLLGLFCTNVAFPPEALMRAPADPAPAPAD
            SSQQASPCTPE DW CWT C PKGCPAETKAEATPRSI RSS NFFLGNKVPAGAEGLS --- SFS EKSL---------

            PASPQHQLAGPAPLLSTPAPEARPVIGALGL
            -------------------------------
```

E.

```
253  GLLNRPN PLLALPPARP HGEPDKDQAV ESAQAEDYSQ LPGE  293
450  T NVAFPPEALR MRAPADPAPA PADPASPQHQ LAGPAPLLST PAPEARPVIG ALGL  504
```

Figure 1.

F.

Homologous patatin phospholipase A (PLA) active site in R1: **S47** and **D166**

```
Active site serine
NA  THIYGASAGA LTA   R1
YF  DVIGGTSTGG LLT   Patatain B2
CA  TYVAGLSGST WYM   cPLA2


Active site aspartic
SLQ GVRYVDGGIS DNLPLYE  R1
ARY EFNLVDGAVA TVGDPAL  Patatin B2
KSK KIHVVDSGL- TFNLPYP  cPLA2
```

Figure 2.

Figure 3.

Figure 4.

Figure 5.

Figure 6.

R1

ORF coding capacity = 504 aa

Clone 12

1   212   959   1362   1726   2122   nt

#11   #1   #2   #12   #3   #13

R1 Expression Constructs

pEXP1-12N

pEXP2-12C

pEXP1-R1N

pEXP2-R1C

pLumio-R1N

pLumio-R1C

6XHis/Xpress   ATG   STOP

V5/6XHis   ATG   STOP

6XHis/Xpress   ATG   V5/6XHis   STOP

Lumio   ATG   STOP

Lumio   ATG   Lumio
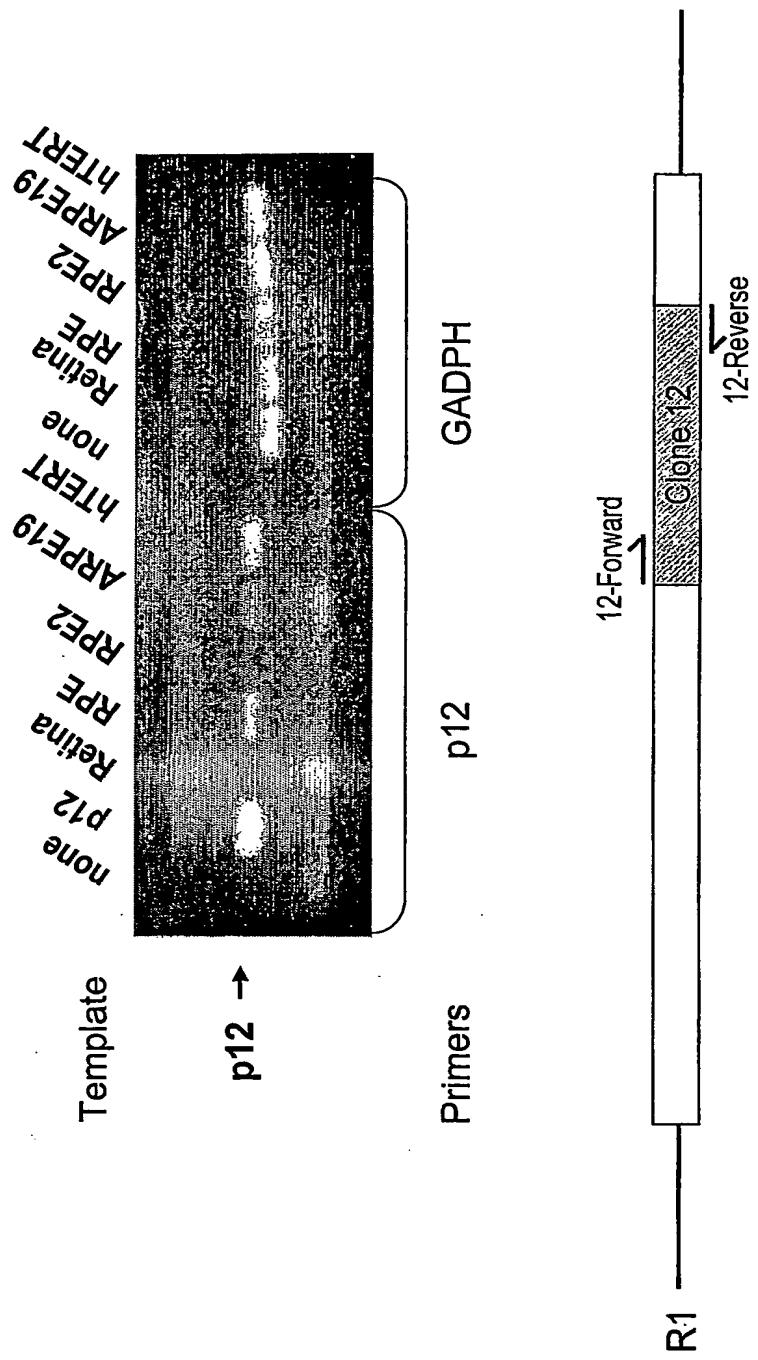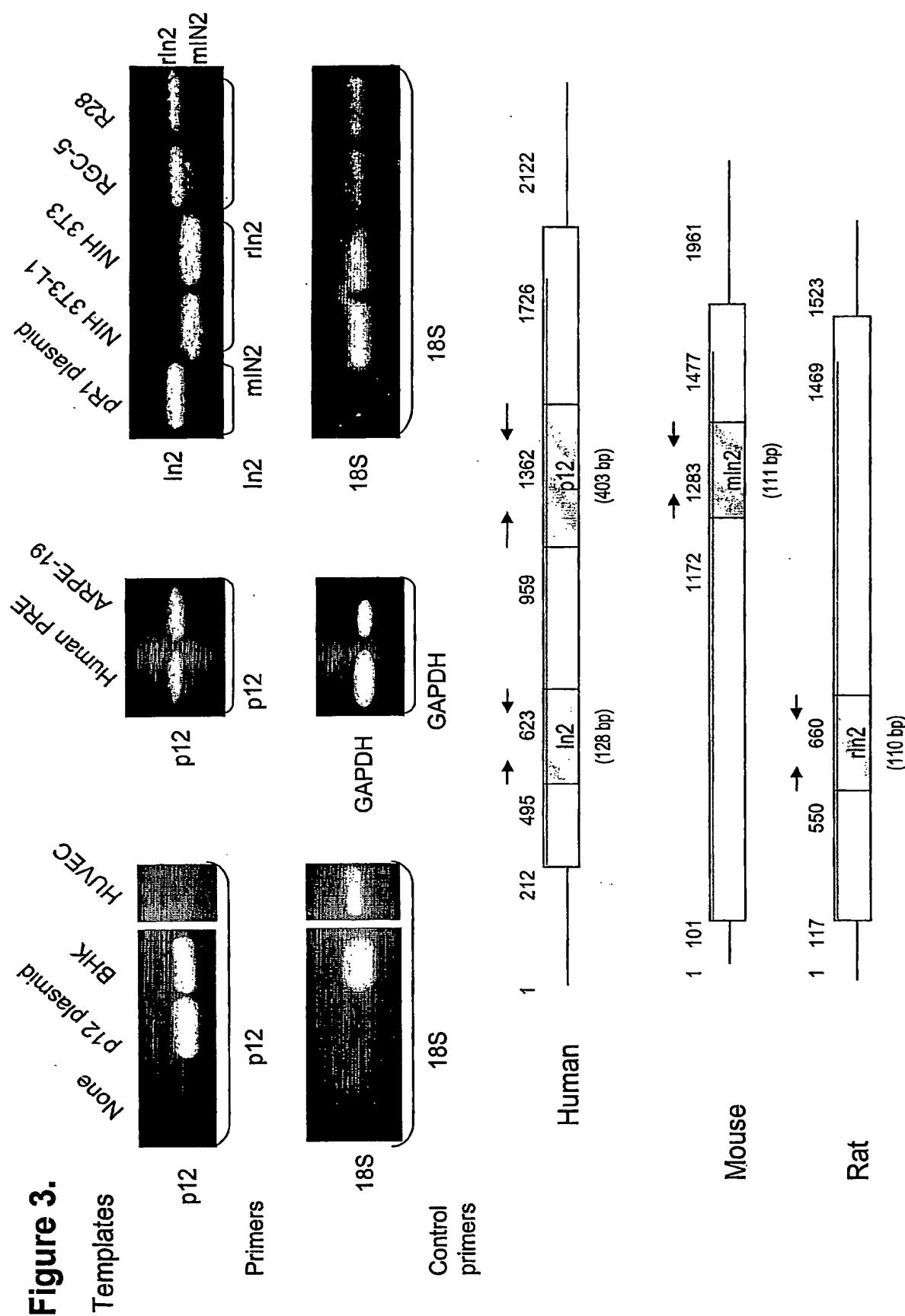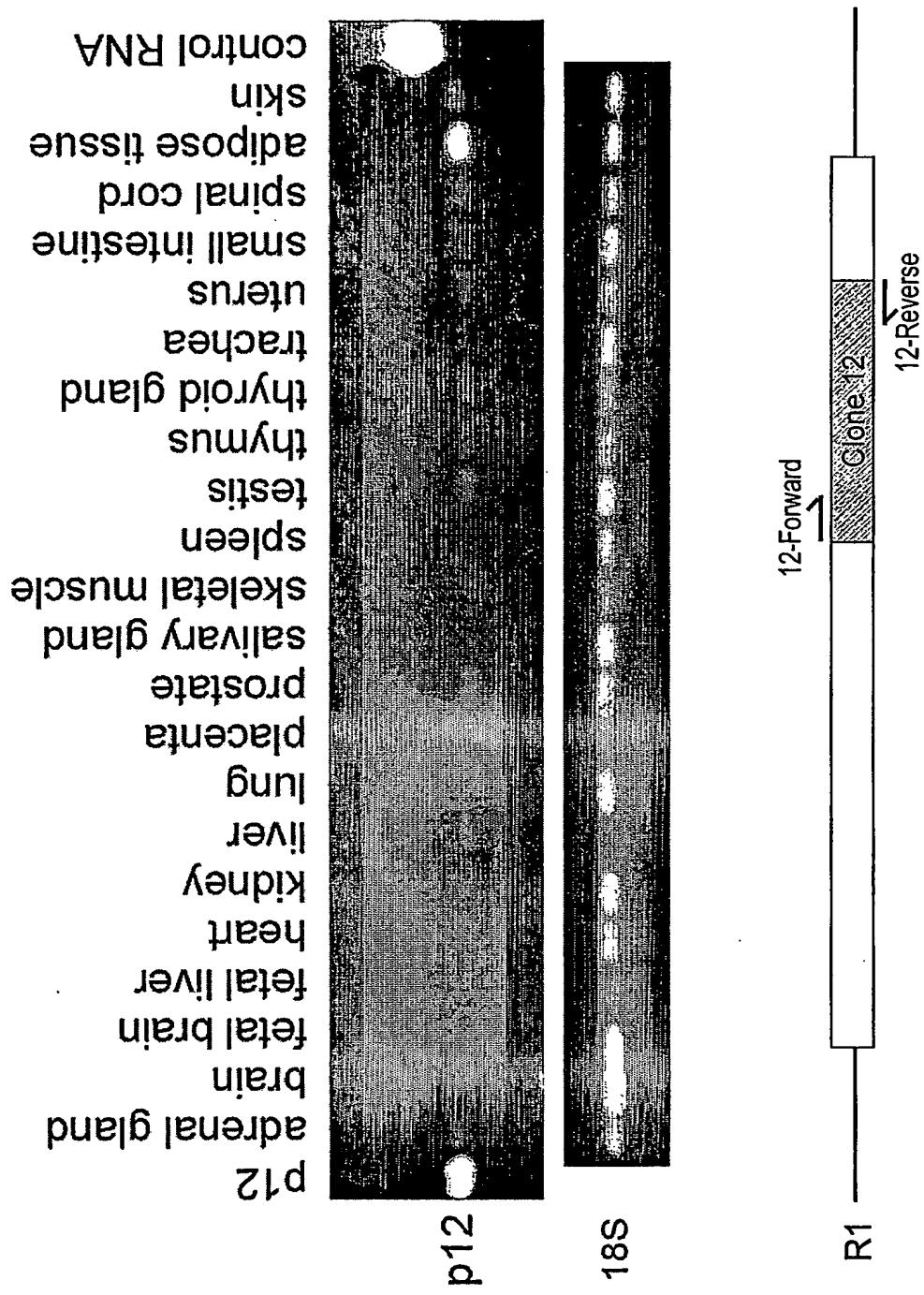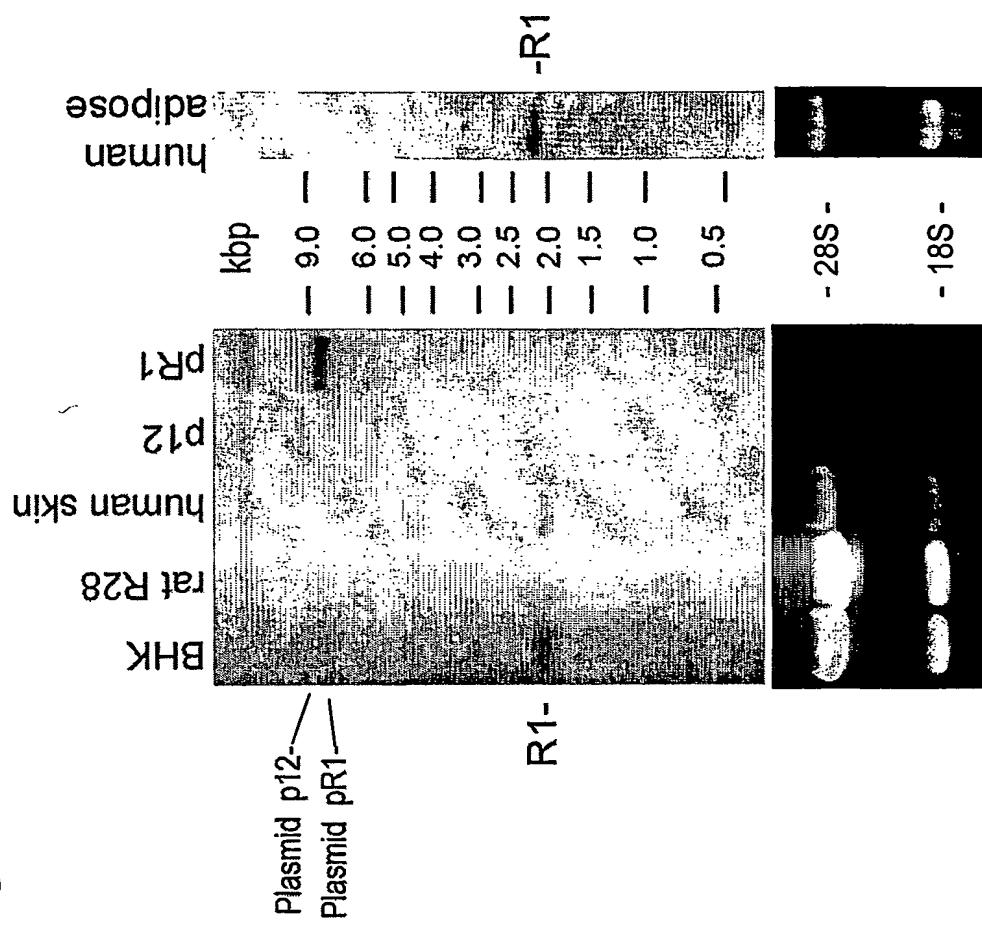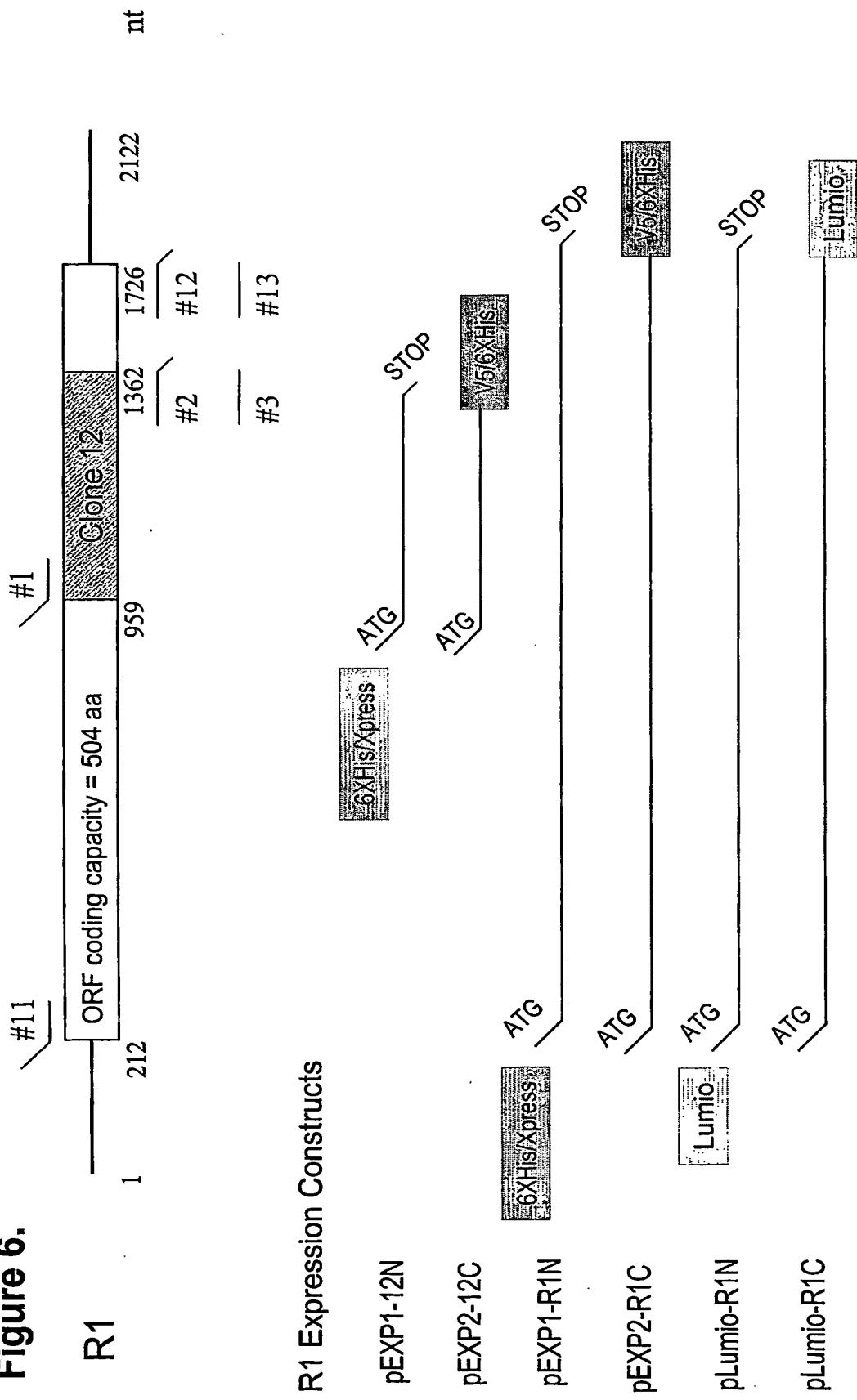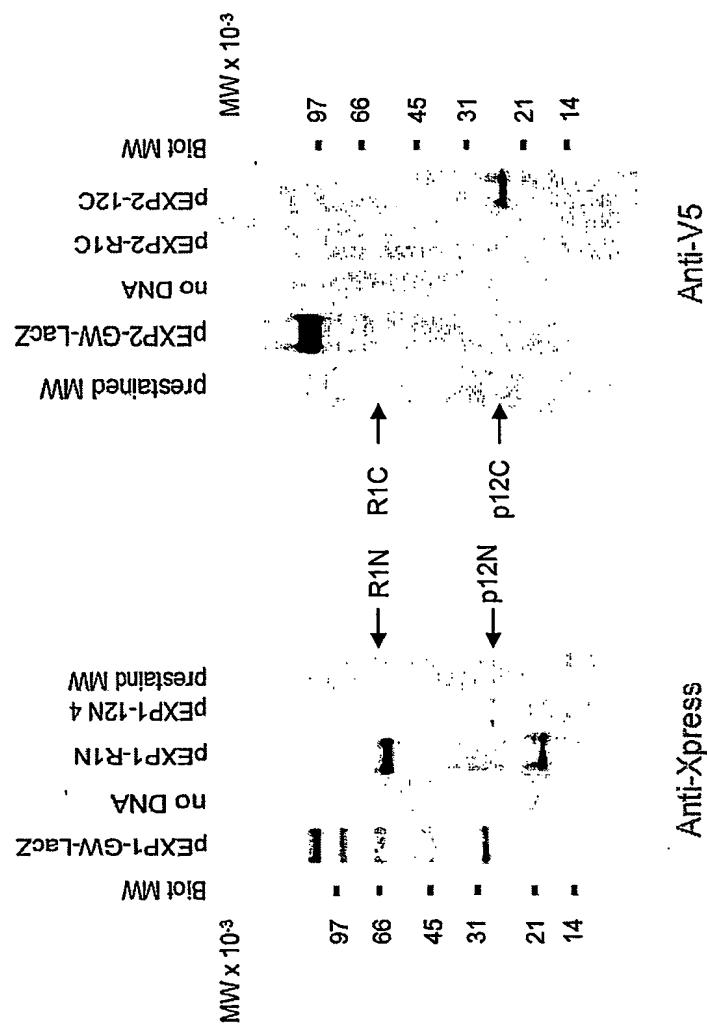
Figure 7.

Figure 8.

A. p12

Chromatogram

SDS-PAGE
(Magic Blue stained gel)

Western (Ab-His)
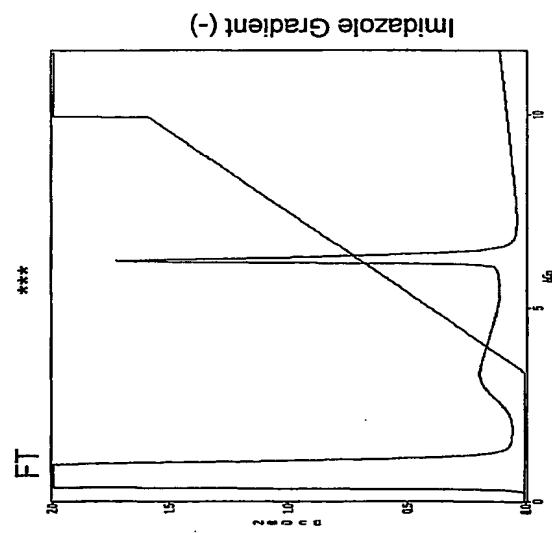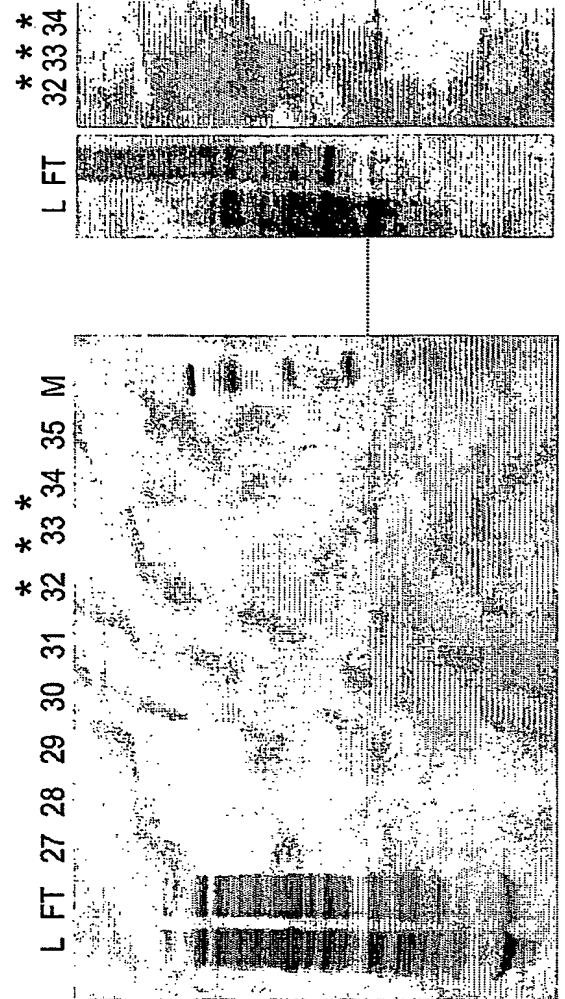
Figure 8.

B. R1

Chromatogram
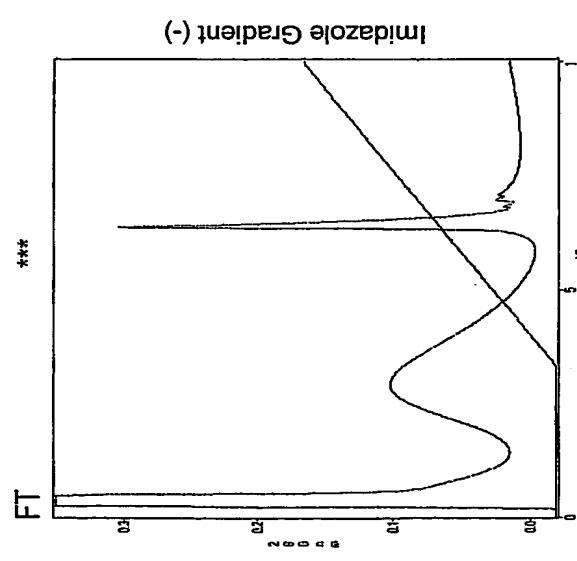
SDS-PAGE (Coomassie Blue stained gel)
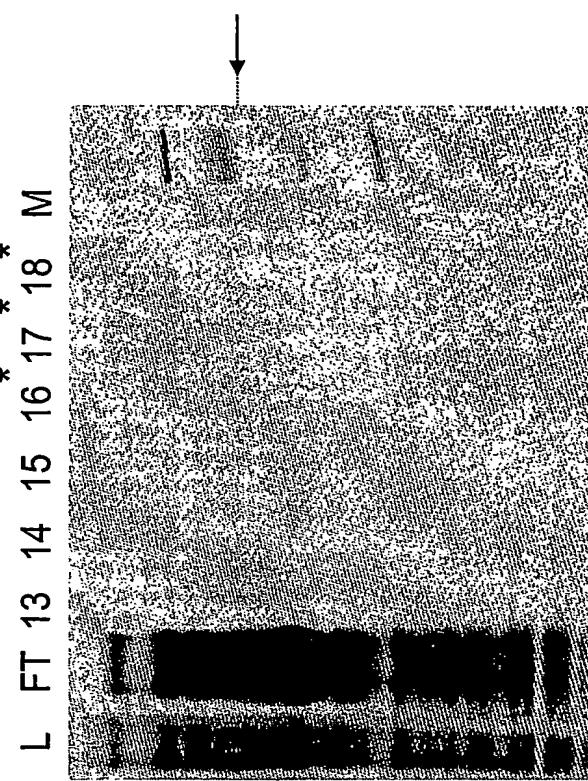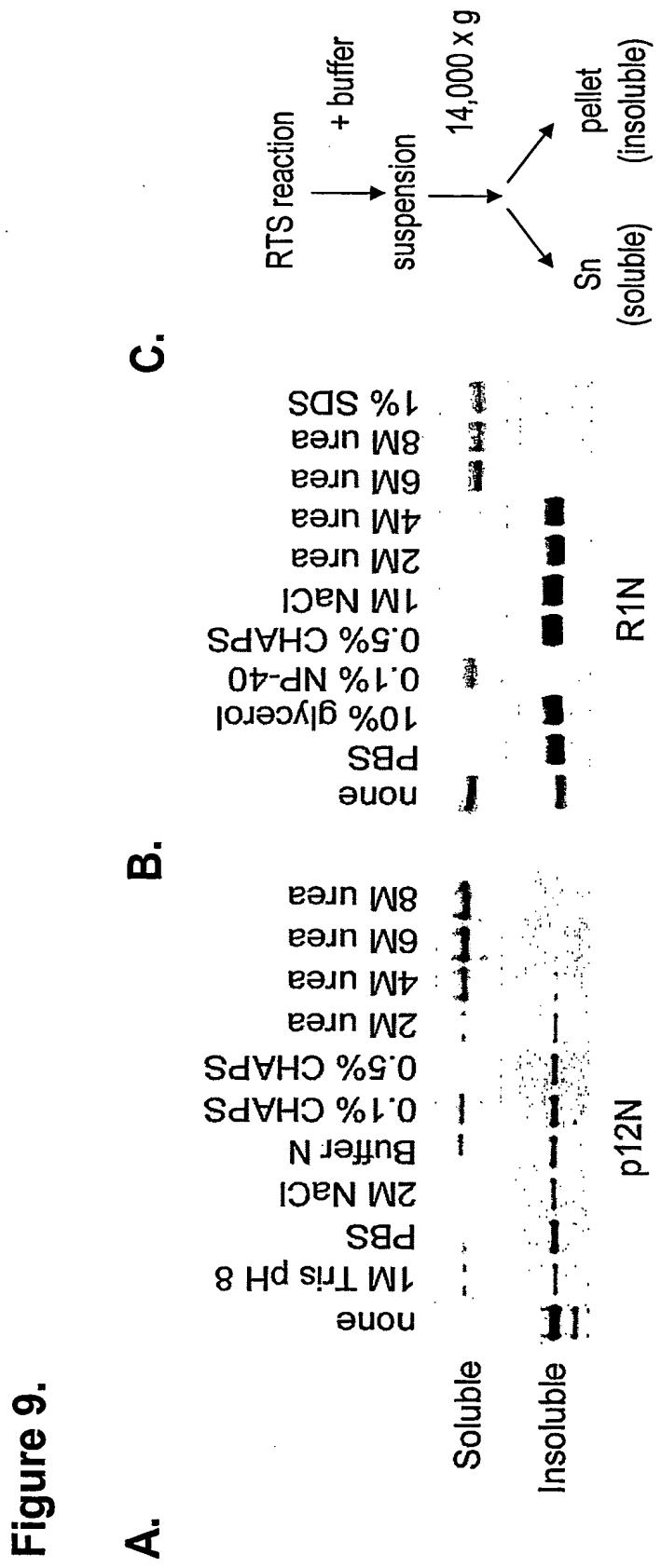
Figure 9.

Figure 10.

A. His-tag pull-down
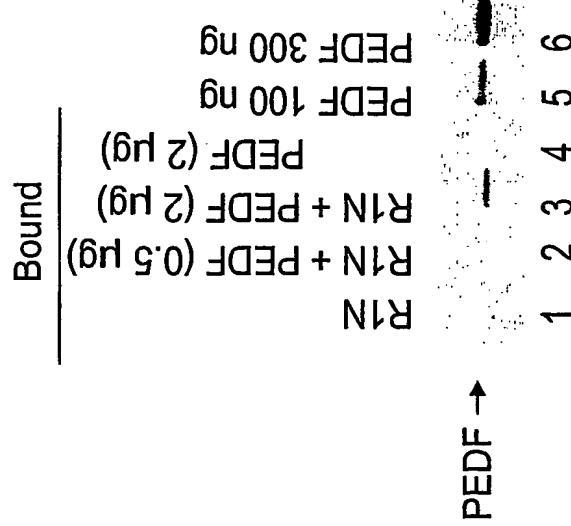
B. complex formation

Figure 11.

A.

B.
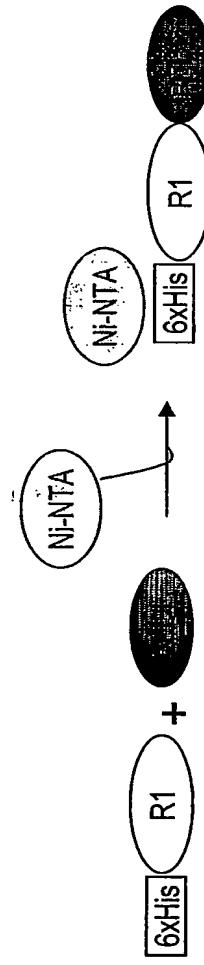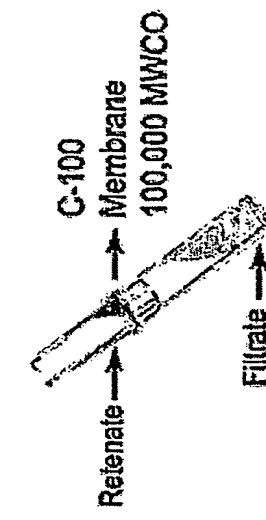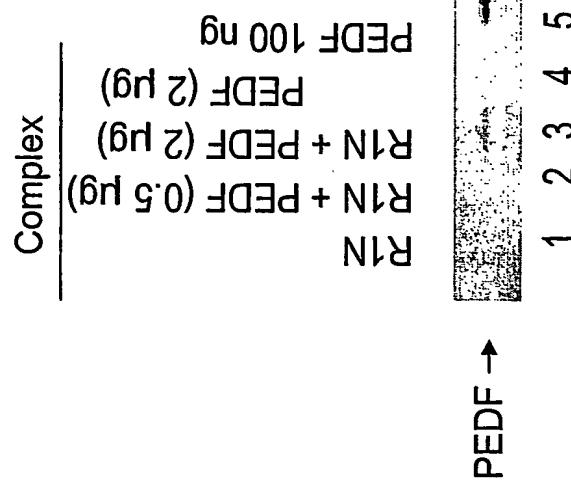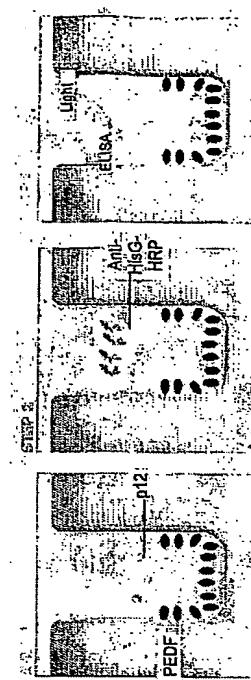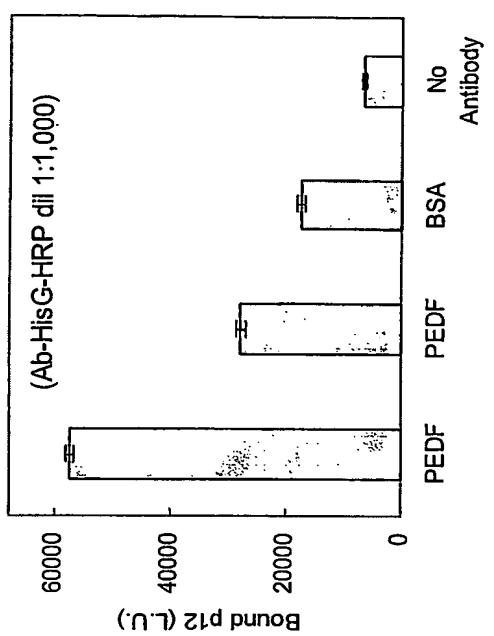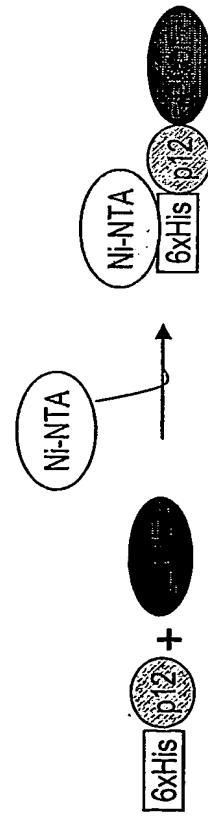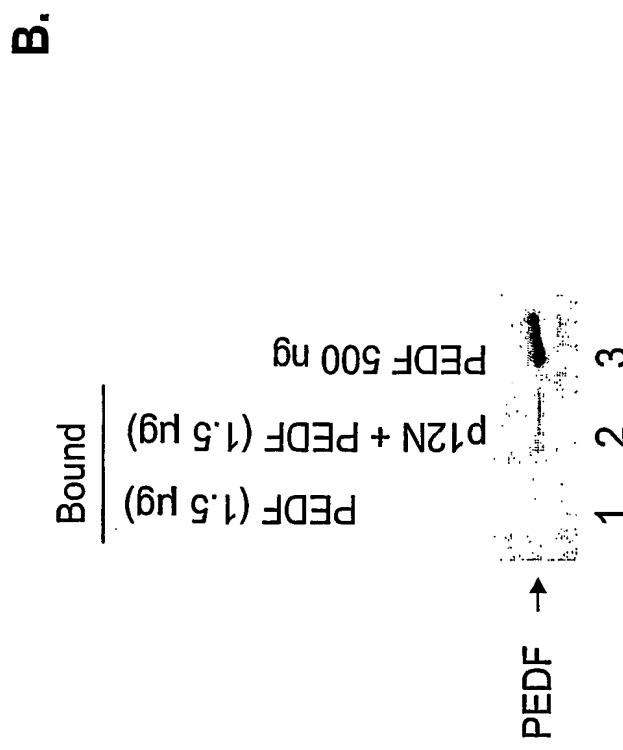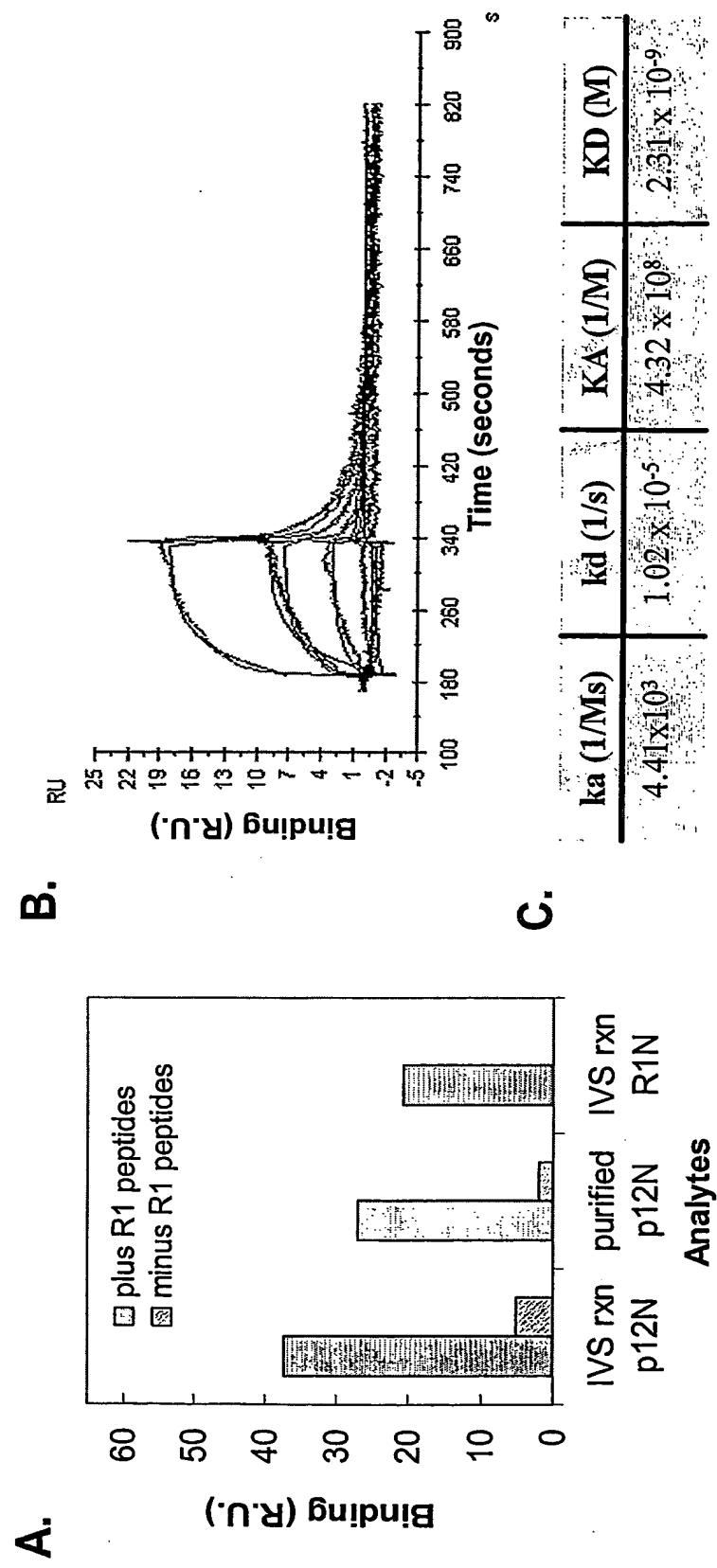
Figure 12.

Figure 13.

A.
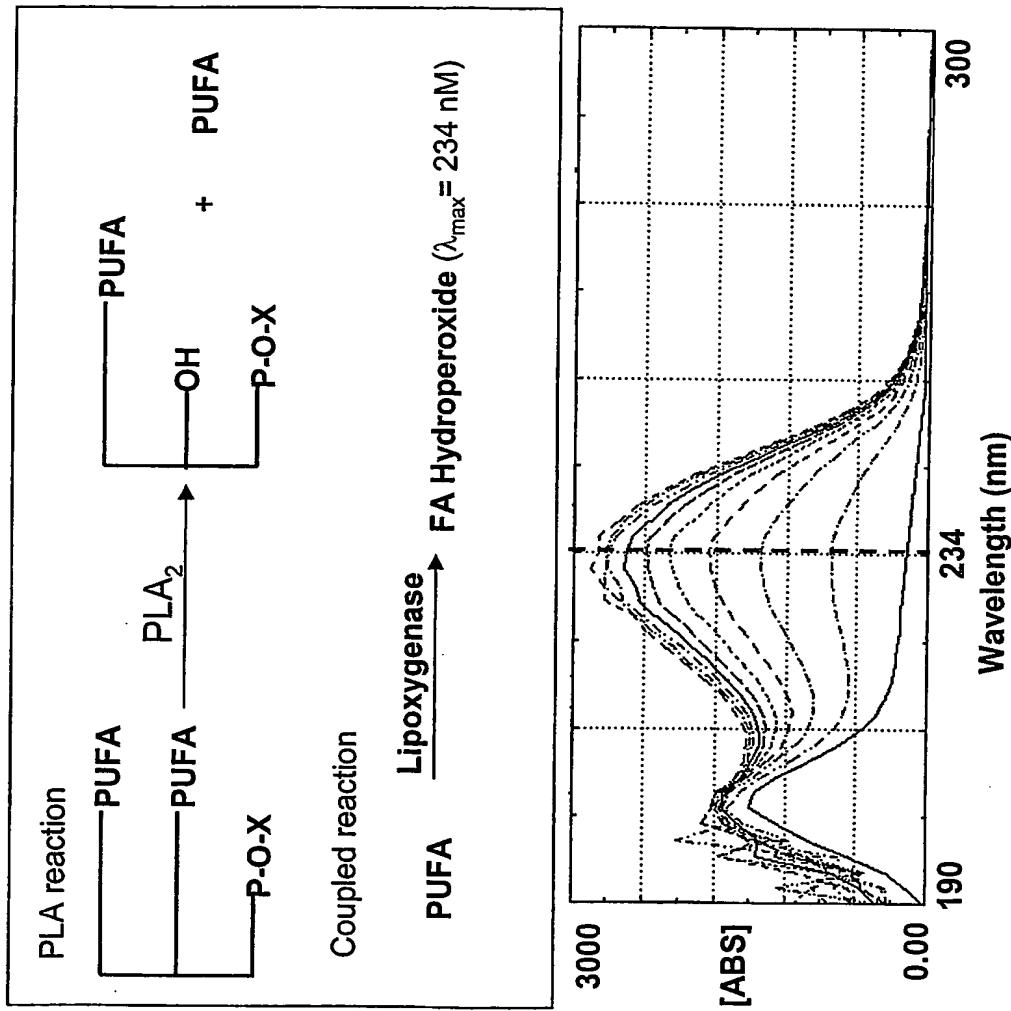
Figure 13.

Figure 14.
A. COS-7 cells
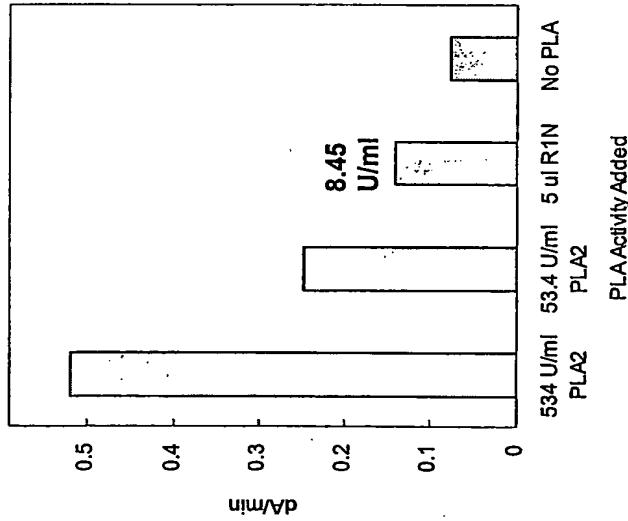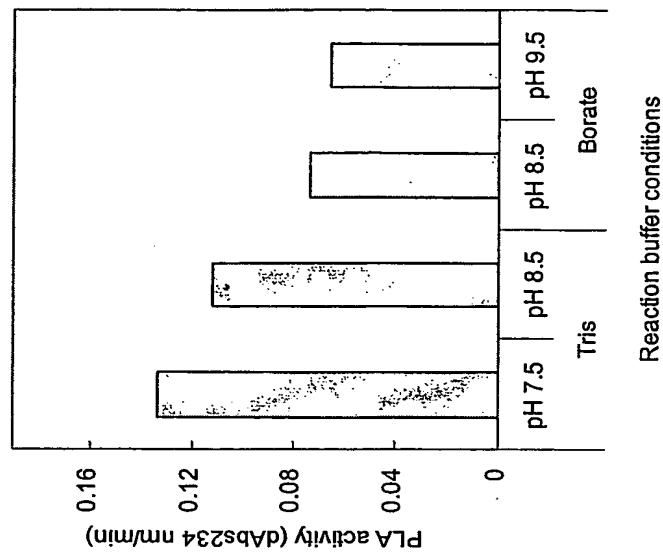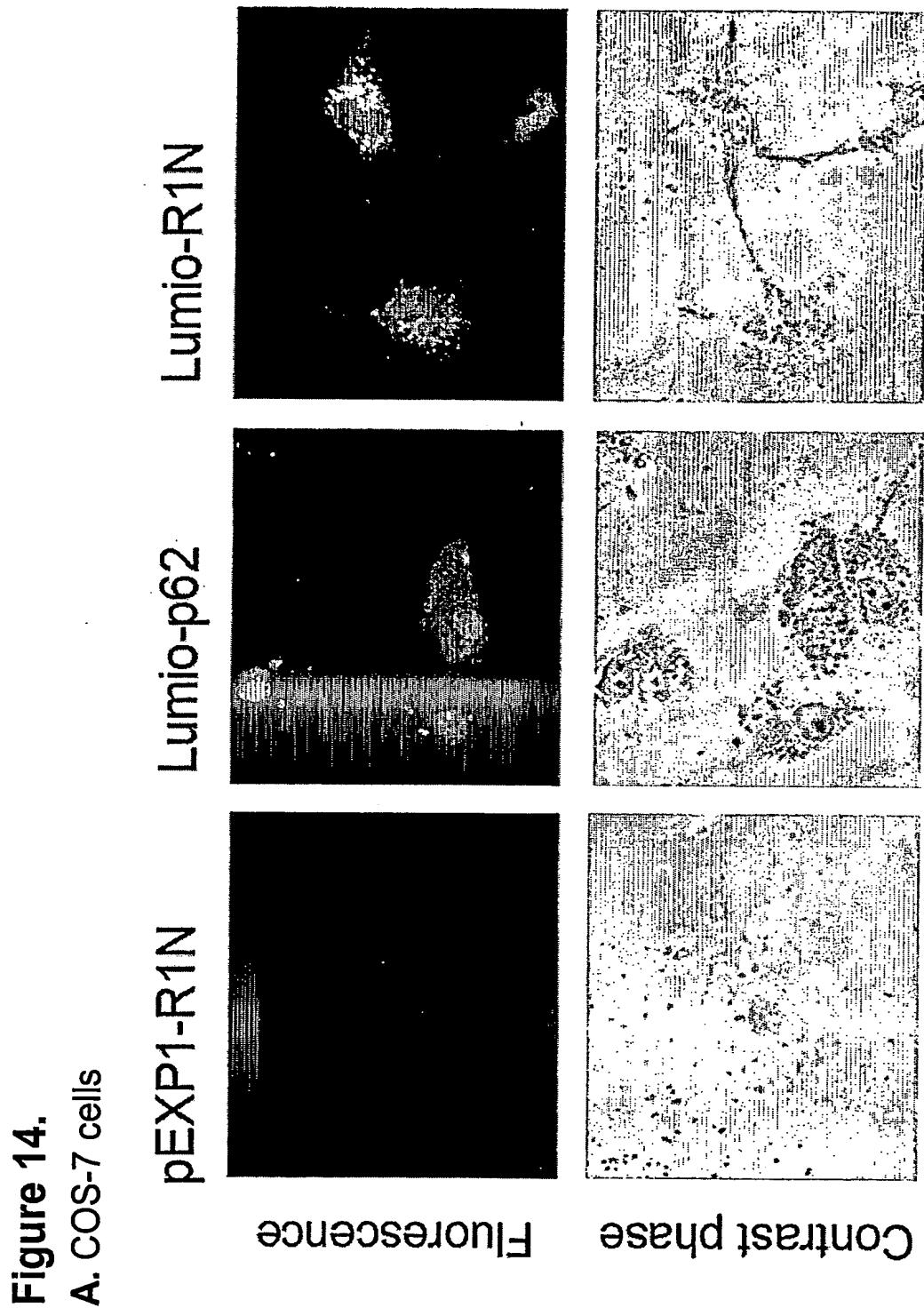
Figure 14.

B. Retinal ganglion RGC-5 cells

Figure 15.

CM LM Lys Cyt Mb Mb M   CM LM Lys Cyt Mb Mb M   CM LM Lys Cyt Mb Mb M
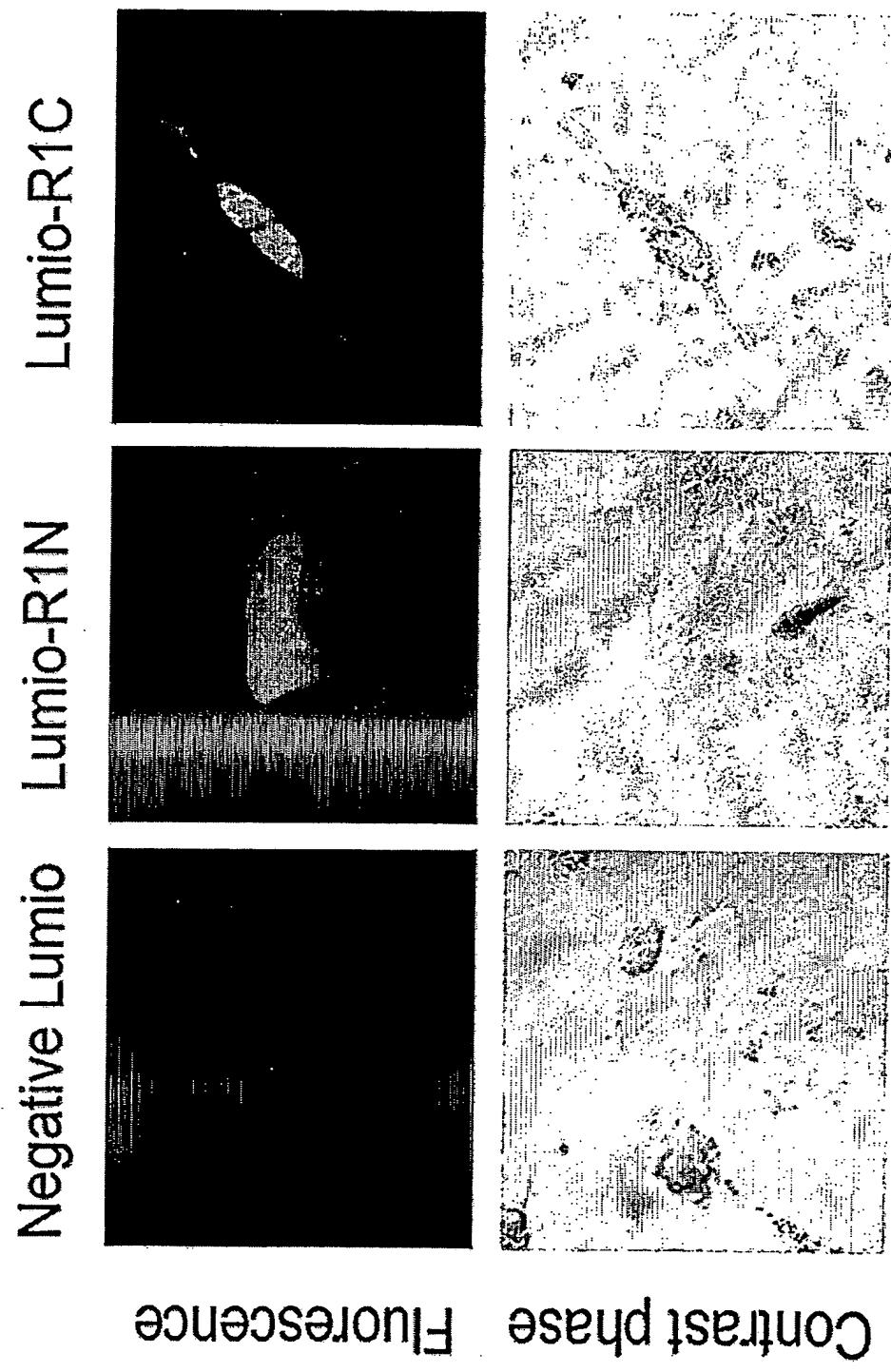
Laser scanned gel   P. Red stained blot   Immunostaining vs. Ab-V5
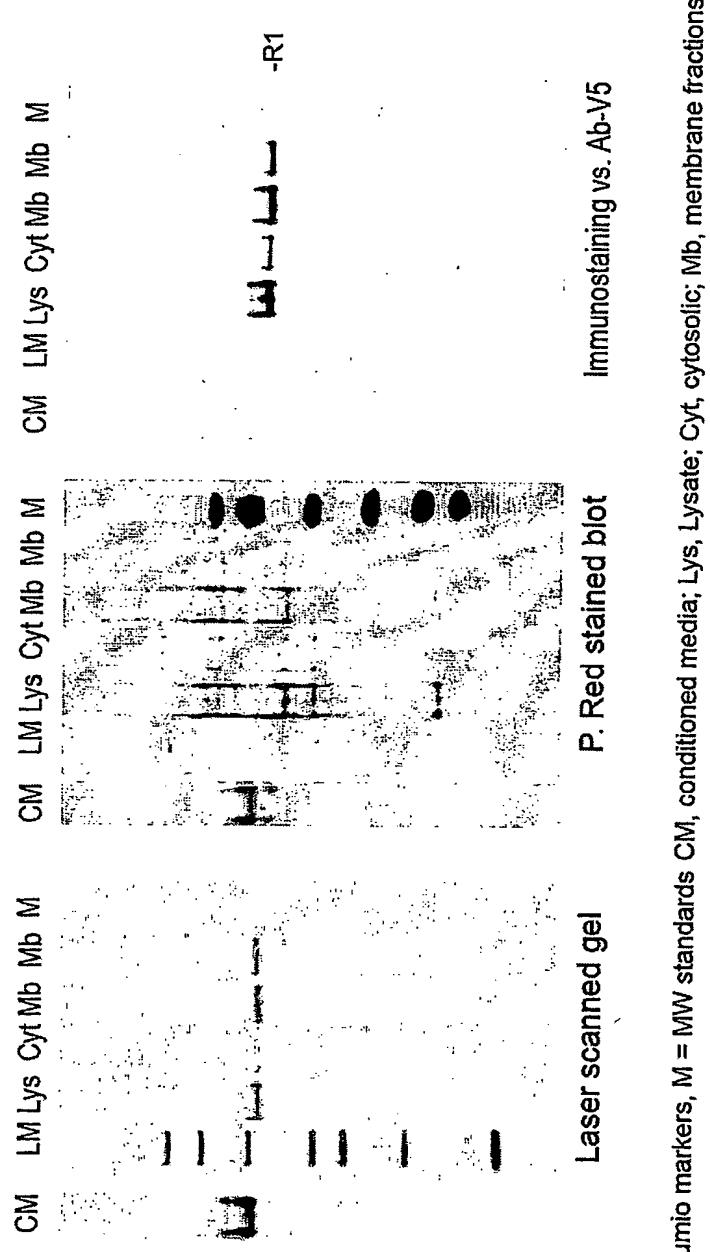
LM= Lumio markers, M = MW standards CM, conditioned media; Lys, Lysate; Cyt, cytosolic; Mb, membrane fractions
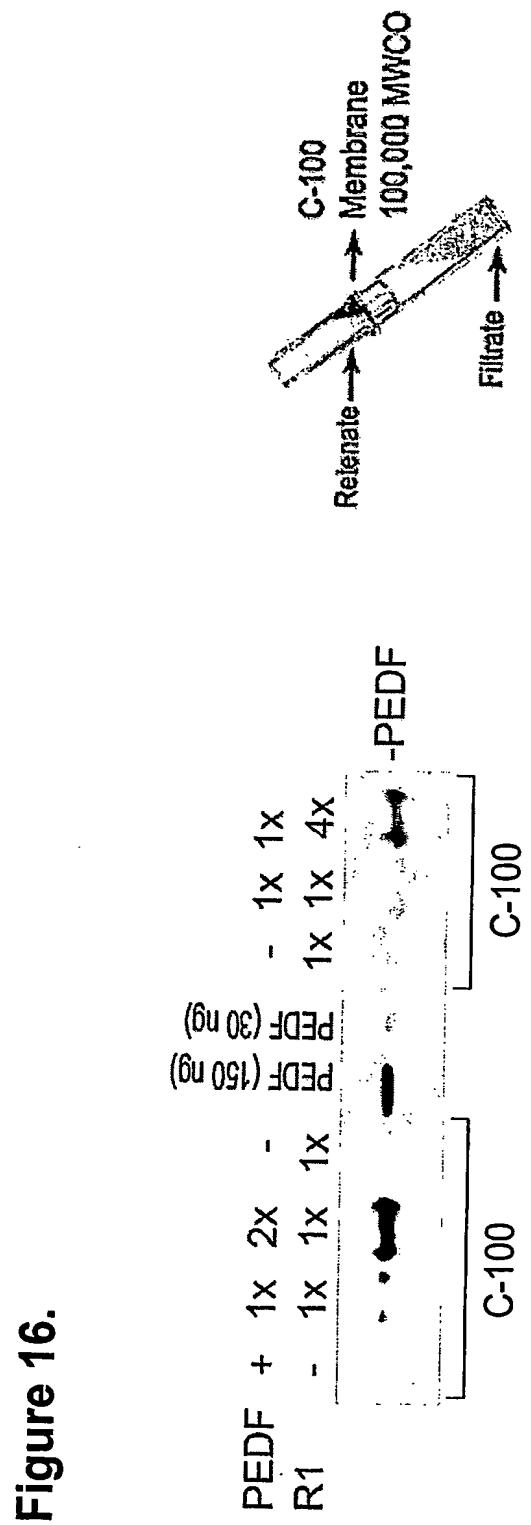
Figure 16.

Figure 17.

A.

Figure 17.

B.

Figure 17.

Figure 18.

Figure 19.

CLUSTAL W (1.82) multiple sequence alignment

```
gi|26327465|dbj|BAC27476.1|     MFPRETKWNISFAGCGFLGVYHIGVASCLREHAPFLVANATHIYGASAGA  50
gi|34861242|ref|XP_341961.1|    MFPRETKWNISFAGCGFLGVYHIGVASCLREHAPFLVANATHIYGASAGA  50
gi|16878147|gb|AAH17280.1|      MFPREKTWNISFAGCGFLGVYYVGVASCLREHAPFLVANATHIYGASAGA  50
                                *****..*************:*************************
```

```
gi|26327465|dbj|BAC27476.1|     LTATALVTGACLGEAGANIIEVSKEARKRFLGPLHPSFNLVKTIRGCLLK  100
gi|34861242|ref|XP_341961.1|    LTATALVTGACLGEAGANIIEVSKEARKRFLGPLHPSFNLVKTIRGCLLK  100
gi|16878147|gb|AAH17280.1|      LTATALVTGVCLGEAGAKFIEVSKEARKRFLGPLHPSFNLVKIIRSFLLK  100
                                *********.******::*******************  **. ***
```

```
gi|26327465|dbj|BAC27476.1|     TLPADCHERANGRLGISLTRVSDGENVIISHFSSKDELIQANVCSTFIPV  150
gi|34861242|ref|XP_341961.1|    TLPADCHTRASGRLGISLTRVSDGENVIISHFSSKDELIQANVCSTFIPV  150
gi|16878147|gb|AAH17280.1|      VLPADSHEHASGRLGISLTRVSDGENVIISHFNSKDELIQANVCSGFIPV  150
                                .****.* :*.********************.***********  ****
```

```
gi|26327465|dbj|BAC27476.1|     YCGLIPPTLQGVRYVDGGISDNLPLYELKNTITVSPFSGESDICPQDSST  200
gi|34861242|ref|XP_341961.1|    YCGLIPPTLQGVRYVDGGISDNLPLYELKNTITVSPFSGESDICPQDSST  200
gi|16878147|gb|AAH17280.1|      YCGLIPPSLQGVRYVDGGISDNLPLYELKNTITVSPFSGESDICPQDSST  200
                                *******:*****************************************
```

```
gi|26327465|dbj|BAC27476.1|     NIHELRVTNTSIQFNLRNLYRLSKALFPPEPMVLREMCKQGYRDGLRFLR  250
gi|34861242|ref|XP_341961.1|    NIHELRITNTSIQFNLRNLYRLSKALFPPEPMVLREMCKQGYRDGLRFLR  250
gi|16878147|gb|AAH17280.1|      NIHELRVTNTSIQFNLRNLYRLSKALFPPEPLVLREMCKQGYRDGLRFLQ  250
                                ******:***************************:***************:
```

```
gi|26327465|dbj|BAC27476.1|     RNGLLNQPNPLLALPPVVPQEEDAEEAAVVEERAGEEDQLQPYRKDRILE  300
gi|34861242|ref|XP_341961.1|    RNGLLNQPNPLLALPPVVPQEEDAEEAAVTEERTGGED-------RILE  292
gi|16878147|gb|AAH17280.1|      RNGLLNRPNPLLALPPARPHGPEDKDQAVESAQAEDYSQLP--GEDHILE  298
                                ******:********. *:   : :: ** . ::   .    :***
```

```
gi|26327465|dbj|BAC27476.1|     HLPARLNEALLEACVEPKDLMTTLSNMLPVRLATAMMVPYTLPLESAVSF  350
gi|34861242|ref|XP_341961.1|    HLPARLNEALLEACVEPKDLMTTLSNMLPVRLATAMMVPYTLPLESAVSF  342
gi|16878147|gb|AAH17280.1|      HLPARLNEALLEACVEPTDLLTTLSNMLPVRLATAMMVPYTLPLESALSF  348
                                *************** .**:*************************:**
```

```
gi|26327465|dbj|BAC27476.1|     TIRLLEWLPDVPEDIRWMKEQTGSICQYLVMRAKRKLGDHLPSRLSEQVE  400
gi|34861242|ref|XP_341961.1|    TIRLLEWLPDVPEDIRWMKEQTGSICQYLVMRAKRKLGDHLPSRLSEQVE  392
gi|16878147|gb|AAH17280.1|      TIRLLEWLPDVPEDIRWMKEQTGSICQYLVMRAKRKLGRHLPSRLPEQVE  398
                                ************************************** ******.****
```

```
gi|26327465|dbj|BAC27476.1|     LRRAQSLPSVPLSCATYSEALPNWVRNNLSLGDALAKWEECQRQLLLGLF  450
gi|34861242|ref|XP_341961.1|    LRRAQSLPSVPLSCATYSEALPNWVRNNLSLGDALAKWEECQRQLLLGLF  442
gi|16878147|gb|AAH17280.1|      LRRVQSLPSVPLSCAAYREALPGWMRNNLSLGDALAKWEECQRQLLLGLF  448
                                ***.**********:* ****.*:*************************
```

```
gi|26327465|dbj|BAC27476.1|     CTNVAFPPDALRMRAPAS--PTAADPATPQDPPGLPPC-------------  486
gi|34861242|ref|XP_341961.1|    CTNVAFPPDALRMRAPAS--PTATDPATPQDPSGLPPC-------------  478
gi|16878147|gb|AAH17280.1|      CTNVAFPPEALRMRAPADPAPAPADPASPQHQLAGPAPLLSTPAPEARPV  498
                                ********:********.  *::.***:**.  . *.
```

```
gi|26327465|dbj|BAC27476.1|     ------
gi|34861242|ref|XP_341961.1|    ------
gi|16878147|gb|AAH17280.1|      IGALGL  504
```

Figure 20. (1 of 4)

CLUSTAL W (1.82) multiple sequence alignment

```
gi|26327464|dbj|AK031609.1|   --------------------------------------------------
gi|34861241|ref|XM_341960.1|  --------------------------------------------------
gi|16878146|gb|BC017280.1|BC01 GGCACGAGGGCGGCCCCAGTCAGACGCAGGCAGCCCCAAAGCCTGAACAG 50


gi|26327464|dbj|AK031609.1|   --------------------------------------------------
gi|34861241|ref|XM_341960.1|  --------------------------------------------------
gi|16878146|gb|BC017280.1|BC01 GCAGGGCCAGACCCAGCTTCTTCGCCTCCGCCAGCGGGGACCCCGAGCTA 100


gi|26327464|dbj|AK031609.1|   --------------------------------------------------
gi|34861241|ref|XM_341960.1|  ------------------TCCTCTGCCTCCCGGCACAGCGTCTCCGCCTCCG 34
gi|16878146|gb|BC017280.1|BC01 GAGCCGCAGCGGGACCTGCCCGGCCCCCGGCTCCAGCGAGCGAGCGGCGA 150


gi|26327464|dbj|AK031609.1|   -----GGAGACCCCAAGGTATCGA-GACTGCGGGACCCACTGCCCGCAGG 44
gi|34861241|ref|XM_341960.1|  CCGGCGGGGACCCCAGGTTATCAA-GACTGCGGGACCCACTGCCCGCAGG 83
gi|16878146|gb|BC017280.1|BC01 GCAGGCGGCTCACAGAGGCCTGGCCGCCCACGGAACCCGGGGCCCGGCGG 200
                              *   *  *    *    *      * *   *** ****   *****  **

gi|26327464|dbj|AK031609.1|   ACATCGAGTCACGGATGTTCCCGAGGGAGACCAAGTGGAACATCTCATTCG 94
gi|34861241|ref|XM_341960.1|  ACGTCTAATCACGGATGTTCCCAAGGGAGACCAAGTGGAACATCTCGTTCG 133
gi|16878146|gb|BC017280.1|BC01 CCGCC--GCCGCGATGTTTCCCCGCGAGAAGACGTGGAACATCTCGTTCG 248
                              *  *     * ******* **   * ****  * *********** ****

gi|26327464|dbj|AK031609.1|   CTGGCTGCGGCTTCCTCGGGGTCTACCACATTGGCGTGGCCTCCTGCCTC 144
gi|34861241|ref|XM_341960.1|  CTGGCTGCGGCTTCCTCGGGGTCTACCACATTGGAGTGGCCTCCTGCCTC 183
gi|16878146|gb|BC017280.1|BC01 CGGGCTGCGGCTTCCTCGGCGTCTACTACGTCGGCGTGGCCTCCTGCCTC 298
                              * ***************** ****** ** * ** ***************

gi|26327464|dbj|AK031609.1|   CGTGAGCACGCGCCCTTCCTGGTGGCCAACGCCACTCACATCTACGGAGC 194
gi|34861241|ref|XM_341960.1|  CGTGAGCACGCGCCCTTCCTGGTGGCCAACGCCACTCACATCTACGGAGC 233
gi|16878146|gb|BC017280.1|BC01 CGCGAGCACGCGCCCTTCCTGGTGGCCAACGCCACGCACATCTACGGCGC 348
                              ** ****************************** *********** **

gi|26327464|dbj|AK031609.1|   CTCGGCAGGGGCGCTCACCGCCACAGCGCTGGTCACTGGGGCCTGCCTGG 244
gi|34861241|ref|XM_341960.1|  CTCGGCAGGGGCGCTTACCGCCACAGCGCTGGTCACTGGGGCCTGCCTGG 283
gi|16878146|gb|BC017280.1|BC01 CTCGGCCGGGGCGCTCACCGGCCACGGCGCTGGTCACCGGGGTCTGCCTGG 398
                              ****** ******** ** ***** *********** **** ********

gi|26327464|dbj|AK031609.1|   GTGAAGCAGGTGCCAACATTATTGAGGTGTCCAAGGAGGCCCGGAAGCGG 294
gi|34861241|ref|XM_341960.1|  GCGAAGCGGGTGCCAACATTATTGAGGTGTCCAAGGAGGCTCGGAAGCGG 333
gi|16878146|gb|BC017280.1|BC01 GTGAGGCTGGTGCCAAGTTCATTGAGGTATCTAAAGAGGCCCGGAAGCGG 448
                              * ** ** ********   * ******** ** **  ***** ********

gi|26327464|dbj|AK031609.1|   TTCCTGGGTCCTCTGCATCCCTCCTTCAACCTGGTGAAGACCATCCGTGG 344
gi|34861241|ref|XM_341960.1|  TTCCTGGGTCCCCTGCACCCCTCCTTCAACCTGGTAAAGACCATCCGTGG 383
gi|16878146|gb|BC017280.1|BC01 TTCCTGGGCCCCCTGCACCCCTCCTTCAACCTGGTAAAGATCATCCGCAG 498
                              ********  ** ***** ***************** **** ******  *

gi|26327464|dbj|AK031609.1|   CTGTCTACTAAAGACCCTGCCTGCTGATTGCCATGAGCGCGCCAATGGAC 394
gi|34861241|ref|XM_341960.1|  TTGTCTACTGAAGACCCTGCCTGCTGATTGCCACACGCGTGCCAGCGGAC 433
gi|16878146|gb|BC017280.1|BC01 TTTCCTGCTGAAGGTCCTGCCTGCTGATAGCCATGAGCATGCCAGTGGGC 548
                              *   ** ** ***  ************** **   **   **** ** *

gi|26327464|dbj|AK031609.1|   GCCTGGGCATCTCCCTGACTCGTGTTTCAGACGGAGAGAACGTCATCATA 444
gi|34861241|ref|XM_341960.1|  GCCTGGGCATCTCCCTGACTCGAGTTTCGGATGGAGAGAATGTCATCATA 483
gi|16878146|gb|BC017280.1|BC01 GCCTGGGCATCTCCCTGACCCGCGTGTCAGACGGCGAGAATGTCATTATA 598
                              ******************* ** ** ** ** ** ***** ***** ***
```

Figure 20. (2 of 4)

```
gi|26327464|dbj|AK031609.1|      TCCCACTTTAGCTCCAAGGATGAGCTCATCCAGGCCAATGTCTGCAGCAC 494
gi|34861241|ref|XM_341960.1|     TCGCACTTTAGCTCCAAGGATGAGCTTATCCAGGCCAATGTTTGCAGCAC 533
gi|16878146|gb|BC017280.1|BC01   TCCCACTTCAACTCCAAGGACGAGCTCATCCAGGCCAATGTCTGCAGCGG 648
                                 ** ***** * ********* ***** ************** ******


gi|26327464|dbj|AK031609.1|      ATTTATCCCGGTGTACTGTGGCCTCATTCCTCCTACCCTCCAAGGGGTGC 544
gi|34861241|ref|XM_341960.1|     TTTTATCCCTGTGTACTGTGGCCTCATTCCTCCTACCCTTCAAGGGGTGC 583
gi|16878146|gb|BC017280.1|BC01   TTTCATCCCCGTGTACTGTGGGCTCATCCCTCCCTCCCTCCAGGGGGTGC 698
                                 ** ***** ********** ***** ***** **** ** *******


gi|26327464|dbj|AK031609.1|      GCTATGTGGATGGCGGCATTTCAGACAACTTGCCACTTTATGAGCTGAAG 594
gi|34861241|ref|XM_341960.1|     GCTATGTGGATGGCGGCATTTCAGACAACTTGCCACTTTATGAGCTGAAG 633
gi|16878146|gb|BC017280.1|BC01   GCTACGTGGATGGTGGCATTTCAGACAACCTGCCACTCTATGAGCTTAAG 748
                                 **** ******* ************** ******* ******* ***


gi|26327464|dbj|AK031609.1|      AATACCATCACAGTGTCCCCATTCTCAGGCGAGAGTGACATCTGCCCTCA 644
gi|34861241|ref|XM_341960.1|     AATACCATCACAGTGTCCCCATTCTCAGGCGAGAGTGACATCTGCCCACA 683
gi|16878146|gb|BC017280.1|BC01   AACACCATCACAGTGTCCCCCTTCTCGGGCGAGAGTGACATCTGTCCGCA 798
                                 ** **************** ***** ***************** ** **


gi|26327464|dbj|AK031609.1|      GGACAGCTCCACCAACATCCACGAGCTTCGCGTCACCAACACCAGCATCC 694
gi|34861241|ref|XM_341960.1|     AGACAGCTCCACCAACATCCACGAACTTCGTATCACCAACACCAGCATCC 733
gi|16878146|gb|BC017280.1|BC01   GGACAGCTCCACCAACATCCACGAGCTGCGGGTCACCAACACCAGCATCC 848
                                  ******************** ** ** *****************


gi|26327464|dbj|AK031609.1|      AGTTCAACCTTCGCAATCTCTACCGCCTCTCGAAGGCTCTCTTCCCGCCA 744
gi|34861241|ref|XM_341960.1|     AATTCAACCTGCGCAATCTCTACCGCCTCTCGAAGGCTCTCTTCCCGCCA 783
gi|16878146|gb|BC017280.1|BC01   AGTTCAACCTGCGCAACCTCTACCGCCTCTCCAAGGCCCTCTTCCCGCCG 898
                                 * ******** ***** ************** ***** **********


gi|26327464|dbj|AK031609.1|      GAGCCCATGGTCCTCCGAGAGATGTGCAAACAGGGCTACAGAGATGGACT 794
gi|34861241|ref|XM_341960.1|     GAGCCCATGGTTCTCCGAGAGATGTGCAAACAGGGCTACCGAGATGGACT 833
gi|16878146|gb|BC017280.1|BC01   GAGCCCCTGGTGCTGCGAGAGATGTGCAAGCAGGGATACCGGGATGGCCT 948
                                 ****** **** ** ************** ***** *** * ***** **


gi|26327464|dbj|AK031609.1|      TCGATTCCTTAGGAGGAATGGCCTACTGAACCAACCCAACCCTTTGCTGG 844
gi|34861241|ref|XM_341960.1|     TCGATTCCTTAGGAGGAATGGCCTACTGAACCAACCCAACCCTTTGCTGG 883
gi|16878146|gb|BC017280.1|BC01   GCGCTTTCTGCAGCGGAACGGCCTCCTGAACCGGCCCAACCCCTTGCTGG 998
                                 ** ** **   * **** ***** ****** ******* *******


gi|26327464|dbj|AK031609.1|      CACTGCCCCCAGTTGTCCCCCAGGAAGAGGATGCAGAGGAAGCTGCTGTG 894
gi|34861241|ref|XM_341960.1|     CACTGCCCCCGGTTGTCCCCCAGGAAGAGGATGCAGAGGAAGCTGCCGTG 933
gi|16878146|gb|BC017280.1|BC01   CGTTGCCCCCGCCCGCCCCCACGG------CCCAGAGGACAAGGACCAG 1042
                                 * ******* * ****** *        ******   *    *


gi|26327464|dbj|AK031609.1|      GTGGAGGAGAGGGCTGGAGAGGAGGATCAATTGCAGCCTTATAGAAAAGA 944
gi|34861241|ref|XM_341960.1|     ACTGAGGAGAGGACTGGAGGGGGAGGATC---------------------- 961
gi|16878146|gb|BC017280.1|BC01   GCAGTGGAGAGCGCCCAAGCGGAGGATTACTCGCAGCTGCCGGGAGAAGA 1092
                                 * ****** *   ** *******


gi|26327464|dbj|AK031609.1|      TCGAATTCTAGAGCACCTGCCTGCCAGACTCAATGAGGCCCTGCTGGAGG 994
gi|34861241|ref|XM_341960.1|     --GGATTCTAGAGCACCTGCCTGCCAGACTCAACGAGGCCCTGCTGGAGG 1009
gi|16878146|gb|BC017280.1|BC01   TCACATCCTGGAGCACCTGCCCGCCCGGCTCAATGAGGCCCTGCTGGAGG 1142
                                 ** ** ********** *** * ***** **** ****************


gi|26327464|dbj|AK031609.1|      CCTGTGTGGAACCAAAGGACCTGATGACCACCCTTTCCAACATGCTACCA 1044
gi|34861241|ref|XM_341960.1|     CCTGTGTGGAACCGAAAGACCTGATGACCACCCTTTCCAACATGCTGCCA 1059
gi|16878146|gb|BC017280.1|BC01   CCTGCGTGGAGCCCACGGACCTGCTGACCACCCTCTCCAACATGCTGCCT 1192
                                 **** ***** ** *  ****** ********** ********** **
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gi|26327464|dbj|AK031609.1|      GTGCGCCTGGCAACGGCCATGATGGTGCCCTATACTCTGCCGCTGGAGAG 1094
gi|34861241|ref|XM_341960.1|     GTGCGCCTGGCCACTGCCATGATGGTACCCTATACTCTGCCACTGGAGAG 1109
gi|16878146|gb|BC017280.1|BC01   GTGCGTCTGGCCACGGCCATGATGGTGCCCTACACGCTGCCGCTGGAGAG 1242
                                 ***** ***** ** ********** ***** ** ***** *******


gi|26327464|dbj|AK031609.1|      TGCAGTGTCCTTCACCATCCGCTTGTTGGAGTGGCTGCCTGATGTCCCTG 1144
gi|34861241|ref|XM_341960.1|     CGCAGTGTCCTTCACCATCCGTTTGTTGGAGTGGCTGCCTGATGTCCCTG 1159
gi|16878146|gb|BC017280.1|BC01   CGCTCTGTCCTTCACCATCCGCTTGCTGGAGTGGCTGCCCGACGTTCCCG 1292
                                  **  *************** *** ************* ** ** ** *


gi|26327464|dbj|AK031609.1|      AAGATATCCGGTGGATGAAAGAGCAGACGGGTAGCATCTGCCAGTATCTG 1194
gi|34861241|ref|XM_341960.1|     AGGATATCCGGTGGATGAAGGAGCAGACAGGTAGCATCTGCCAGTATCTG 1209
gi|16878146|gb|BC017280.1|BC01   AGGACATCCGGTGGATGAAGGAGCAGACGGGCAGCATCTGCCAGTACCTG 1342
                                 * ** ************** ******* ** ************** ***


gi|26327464|dbj|AK031609.1|      GTGATGAGGGCCAAGAGGAAATTGGGTGACCATCTGCCTTCCAGACTGTC 1244
gi|34861241|ref|XM_341960.1|     GTGATGAGGGCCAAGAGGAAATTGGGTGACCATCTACCTTCCAGACTGTC 1259
gi|16878146|gb|BC017280.1|BC01   GTGATGCGCGCCAAGAGGAAGCTGGGCAGGCACCTGCCCTCCAGGCTGCC 1392
                                 ****** * ********** ****     ** ** ** ***** *** *


gi|26327464|dbj|AK031609.1|      TGAGCAGGTGGAACTGCGACGTGCCCAGTCTCTGCCCTCTGTGCCACTGT 1294
gi|34861241|ref|XM_341960.1|     TGAGCAGGTGGAGCTGCGGCGTGCCCAGTCTCTGCCGTCTGTGCCACTGT 1309
gi|16878146|gb|BC017280.1|BC01   GGAGCAGGTGGAGCTGCGCCGCGTCCAGTCGCTGCCGTCCGTGCCGCTGT 1442
                                  *********** ***** ** * ****** ***** ** ** *** ****


gi|26327464|dbj|AK031609.1|      CTTGCGCCACCTACAGTGAGGCCCTACCCAACTGGGTACGAAACAACCTC 1344
gi|34861241|ref|XM_341960.1|     CTTGCGCCACCTACAGTGAGGCACTGCCCAACTGGGTACGAAACAACCTC 1359
gi|16878146|gb|BC017280.1|BC01   CCTGCCGCCGCCTACAGAGAGGCACTGCCCGGCTGGATGCGCAACAACCTC 1492
                                 * ***** ******* ***** ** *** **** * ** *********


gi|26327464|dbj|AK031609.1|      TCACTGGGGGACGCGCTGGCCAAGTGGGAAGAATGCCAGCGTCAGCTACT 1394
gi|34861241|ref|XM_341960.1|     TCACTGGGGGACGCGCTGGCCAAGTGGGAAGAATGCCAGCGTCAGCTACT 1409
gi|16878146|gb|BC017280.1|BC01   TCGCTGGGGGACGCGCTGGCCAAGTGGGAGGAGTGCCAGCGCCAGCTGCT 1542
                                 ** ************************** ** ******** ***** **


gi|26327464|dbj|AK031609.1|      GCTGGGTCTCTTCTGCACCAATGTGGCCTTCCCGCCGGATGCCTTGCGCA 1444
gi|34861241|ref|XM_341960.1|     GCTGGGTCTCTTCTGCACCAATGTGGCCTTCCCGCCTGATGCCTTGCGCA 1459
gi|16878146|gb|BC017280.1|BC01   GCTCGGCCTCTTCTGCACCAACGTGGCCTTCCCGCCCGAAGCTCTGCGCA 1592
                                 *** ** ************* ************* ** ** ******


gi|26327464|dbj|AK031609.1|      TGCGCGCACCTGCCAGCCC------CACTGCCGCAGATCCTGCCACCCCA 1488
gi|34861241|ref|XM_341960.1|     TGCGCGCACCTGCCAGCCC------CACCGCCACAGATCCTGCCACCCCA 1503
gi|16878146|gb|BC017280.1|BC01   TGCGCGCACCCGCCGACCCGGCTCCCGCCCCCGCGGACCCAGCATCCCCG 1642
                                 ********** *** ***     * * ** * ** ** ** ****


gi|26327464|dbj|AK031609.1|      CAGGATCCAC----CTGGCCTCCCGCCTTGCTGAGAATCACCATTCCCAC 1534
gi|34861241|ref|XM_341960.1|     CAGGATCCAT----CTGGCCTCCCACCTTGCTGA---------------- 1533
gi|16878146|gb|BC017280.1|BC01   CAGCACCAGCTGGCCGGGGCCTGCCCCCTTGCTGAGCACCCTGCTCCCGA 1692
                                 *** * *        * ***** ** *********


gi|26327464|dbj|AK031609.1|      ATCGCCCGGCTACCAGCCAAGCTCCAAGTTGTCCTGCCCCACTAAGAGGA 1584
gi|34861241|ref|XM_341960.1|     --------------------------------------------------
gi|16878146|gb|BC017280.1|BC01   G--GCCCGGCCCGTGATCGGG---------GCCCTGGGGCTGTGAGA--- 1728


gi|26327464|dbj|AK031609.1|      GCCCCGGGGTGGAACAAGATCCTGTCTGCCCCGGCTCTCCCCCTTACATG 1634
gi|34861241|ref|XM_341960.1|     --------------------------------------------------
gi|16878146|gb|BC017280.1|BC01   -CCCCGACCCTCTCGAGGAACC---CTGCCTGAGACGCCTCCATTAC-CA 1773


gi|26327464|dbj|AK031609.1|      CTGTGGAATGAGGACATAGGACCCTGCACAGCTGCAAGTGGGCTTTCGAT 1684
gi|34861241|ref|XM_341960.1|     --------------------------------------------------
gi|16878146|gb|BC017280.1|BC01   CTGCGCAGTGAGATGAGGGGACTCACAGTTGCCAAGAG-GGGTCTTTGCC 1822
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gi|26327464|dbj|AK031609.1|        GTGAAACCTTTCACCAGCCACTCACTATGCTACTCCTGGTGGGGAGGGAT 1734
gi|34861241|ref|XM_341960.1|       --------------------------------------------------
gi|16878146|gb|BC017280.1|BC01     GTGGGCCCCCTCGCCAGCCACTCACCA-GCTGCATGCACTGAGAGGGGAG 1871


gi|26327464|dbj|AK031609.1|        GGGGAGTCGCCCTCCCCCGGAGCCCACAGAGCCCTCCCCCGTCACGTC--- 1782
gi|34861241|ref|XM_341960.1|       --------------------------------------------------
gi|16878146|gb|BC017280.1|BC01     GTTTCCACACCCCTCCCCTGGGCCGCTGAGGCCCCGCGCACCTGTGCCTT 1921


gi|26327464|dbj|AK031609.1|        ACCTGTGCCTTACTCCTGCCCACCA--CCTTTTCAGTGCAGGGTCAGTCT 1830
gi|34861241|ref|XM_341960.1|       --------------------------------------------------
gi|16878146|gb|BC017280.1|BC01     AATCTTCCCTCCCCTGTGCTGCCCGAGCACCTCCCCCGCCCCTTTACTCC 1971


gi|26327464|dbj|AK031609.1|        TAAGAACTCCACATCTGCTGCTGC-TCCCTGGTGTCCAAGTTTCCTTGCA 1879
gi|34861241|ref|XM_341960.1|       --------------------------------------------------
gi|16878146|gb|BC017280.1|BC01     TGAGAACTTTGCAGCTGCCCTTCCCTCCCCGTTTTTCATGGCCTGCTGAA 2021


gi|26327464|dbj|AK031609.1|        GA--GTGTGTGAAGAATTATTTATTTTTGCCAAAGCAGATCTAATAAAAG 1927
gi|34861241|ref|XM_341960.1|       --------------------------------------------------
gi|16878146|gb|BC017280.1|BC01     ATATGTGTGTGAAGAATTATTTATTTTCGCCAAAGCACATGTAATAAATG 2071


gi|26327464|dbj|AK031609.1|        CCACAGCTCAGCTTCTGCCTTCCTCACTTCTGCATGCT------------ 1965
gi|34861241|ref|XM_341960.1|       --------------------------------------------------
gi|16878146|gb|BC017280.1|BC01     CTGCAGCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2121


gi|26327464|dbj|AK031609.1|        -
gi|34861241|ref|XM_341960.1|       -
gi|16878146|gb|BC017280.1|BC01     A 2122
```